



Figure 16: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-b1b2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1 3768 bp
Sequence 2: Mi1.2 3774 bp
Sequence 3: Rpi-b1b2 3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2 Score: 68908
Group 2: Sequences: 3 Score: 65855
Alignment Score 66872
CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mi1.1	ATGGAAAAACGAAAGATAATGAAGAAGCAAAACAACCTATTGGTGTATTTCCTGCTCTT	60
Mi1.2	ATGGAAAAACGAAAAGATATTAAGAAGCAAAACAACCTATTGGTGTATTTCCTGCTCTT	60
Rpi-b1b2	ATGGAAAAACGAAAAGATAATGAAGAAGCAAAACAACCTATTGGAGGTCAATTTCCTGCTCTT	60
	*****	*****

Mi1.1	AGCAAGGACATGCCGATGTTCTGGTTTCCTAGAGA-----	ATGAGGAAATCAA 111
Mi1.2	AGCAAGGACATGCCAATGTCTTAATTTCCTAGAGA-----	ATGAGGAAATCAA 111
Rpi-blb2	CGCAAGGGATGCCAATGTCTGGATTTCCTAGAGAAGATTAAAGAATGAAAGATCAA 120	
	*****	*****
Mi1.1	AAAGCTCTGACAAAGATCAAGTTGAAAAGATAAAATTGAGCATTATTGTACA 171	
Mi1.2	AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAATTGAAATGGCATTATTGTACA 171	
Rpi-blb2	AGGCCTGTTGATGTGGATCTGATTGAAAGCCTGAAGCTGACATTATTGTACA 180	
	*****	*****
Mi1.1	TATGTTCAGCTTCTTGTGTTCCGATTGAGCAGTTGAAAGATATAATGACTAGAAAAAGA 231	
Mi1.2	TATGTTCAGCTTCTTATTCCGATTGAGCAGTTGAAAGATATAATGACTAGAAATAGA 231	
Rpi-blb2	TATGTTCCAGCTTCTTATTCCGATTGAGCAGTTGAAAGATATAATGACTAGAAAAAGA 240	
	*****	*****
Mi1.1	CAAGAGGTGAGAAATCTGCTCAACCACCTTTGGATGATGATG-----	274
Mi1.2	CAAGAGGTGAGAAATCTGCTCAATCACTTTGGATGATGATG-----	274
Rpi-blb2	CAAGAGGTGAGAAATCTGCTCAACCAATTGGATGATGATGGCAAAAGACGTCGGGTGT 300	
	*****	*****
Mi1.1	-----TCTTTACTAGCCTCACCAAGTAATATGGATGACTGTATCAGCTTGTATCATCGT 327	
Mi1.2	-----TCCTTACTAGCCTCACCAAGTAATATGGATGACTGTATCAGCTTGTATCATCGT 327	
Rpi-blb2	AAATATGTCCTTACAGCCTCACCAAGTAATATGGATGACTGTATAAGCTTGTATCATCGT 360	
	*****	*****
Mi1.1	TCTTATAAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCCTCTTGAATCTC 387	
Mi1.2	TCTTATAAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCCTCTTGAATCTG 387	
Rpi-blb2	TCT---AAATCAGATGCCACCATGATGGATGAGCAATTGGCTTCCCTCTTGAATCTC 417	
	*****	*****

Mi1.1	TATCATCTATCCAAGCATTACCGCTGAAAGATAATTCCCTGGAGTGACTCAATATGAAGTT	447
Mi1.2	TATCATCTATCCAAGCATTACCGCTGAAAGATAATTCCCTGGAGTGACTCAATATGAAGTT	447
Rpi-blb2	TCTCATCTATCCAAGCATTACCGCTGAAAGATAATTCCCTGGAGTGACTCAATATGAAGTT	477
	*****	*****
Mi1.1	CTTCAGAATATATGTGGCAACATAAGAGATTCCATGGGTTGATAAGTGAATGGTTGCATT	507
Mi1.2	CTTCAGAATATGTGGCAACATAAGAGATTCCATGGGTTGATAAGTGAATGGTTGCATT	507
Rpi-blb2	CTTCAGAATATGTGGCAACATAAGAGATTCCATGGGTTGATAAGTGAATGGTTGCATT	537
	*****	*****
Mi1.1	AAGCATGAGATGGTTGAGAATGTCCTTCACACTCATGGCTGACAGAGTAGGAA	567
Mi1.2	AAGCATGAGATGGTTGAGAATGTCCTTCACCTCATGGCTGAAAGAGTAGGAA	567
Rpi-blb2	AAGCATGAGATGGTTGAGAATGTCCTTATCTCTGGCTCAACTGTGGCTGAGAGTAGGAA	597
	*****	*****
Mi1.1	CACTTCCTTGGGATGAGACTTGATGAAAGACTCTCGACTCTCCGAGCTAGATGAGGAT	627
Mi1.2	CACTTCCTTGGGAGGGATCAGACTGATGAAAGACTCTCGCTCTCGAGCTAGATGAGGAT	627
Rpi-blb2	CGCTTCCTTGGGAGGGATCAGGCTGATGAAAGACTCTCAACTCTCCGAGCTAGATGAGGAT	657
	*****	*****
Mi1.1	GAAACAAATGATAGAGACTCTCGACTTTCAAGCTAGCACATCTACTCTGAAGATTCAGTT	687
Mi1.2	GAAACAAATGATAGAGACTCTCGACTTTCCAGCTAACACATCTACTCTGAAGATTCAGTT	687
Rpi-blb2	GATCAGAATGATAAAGACCTCAACTCTCAAGCTAGCACATCTACTCTGAAGATTCAGTT	717
	*****	*****
Mi1.1	CCGGTTGAACTGGAGGTTATACACATATGTTATACAAACTTGAAGGCTTCAAACCTCAGCT	747
Mi1.2	CCAACTGAACTGGAGGTTATGCACATATGTTATACAAATTGAAAGCTTCAAACCTCAGCA	747
Rpi-blb2	CCAACTGAACTGGAGGTTATGCACATATGTTATACAAACTTGAAGGCTTCAAACCAACA	777
	*****	*****
Mi1.1	GAAGTTGGGAACTCTTCAATTAAAGCAGCTCTAGAAAACCTCCAGATAATTCTGAGGGAAATAT	807

Mi1.2	GAAAGTTGGACCGCTTCATTAAGAAGCTCCTGGAAACCTAACCGGATATTCTCAGAGAATAT	807
Rpi-blb2	GAAATTGGACCGCTTCATTAAGAAGCTCCTGGAAACCTAACCGGACATTCTCAGAGAATAT	837
	***** *	
Mi1.1	CTAATTCCCTCTGCAAGAGCACATGGTAACTGTATTACCCCTAGCACTTCAGGGGCTCGA	867
Mi1.2	ATCATTCAGCTACAAGGCCATATGTTAACTGTATTCCCCCTAGCACTTCTAGGGGCTCGA	867
Rpi-blb2	CTGATTCACTCTACAAGGCCATATGATAACTGTATTACCCCTAACACTTCAGGGGCTCGA	897
	* *	
Mi1.1	AACATTCACTGTCATGATGGATTCCATTACTTATTCTGATATGCC --- CAAGGAC	924
Mi1.2	AACATTCACTGTCATGATGGATTCCATTACTTATTCTGATATGCC --- CAAGGAC	924
Rpi-blb2	AACATTCACTGTCATGATGGATTCCATTGTATTCTGATATGCCGCCAAGGAC	957
	***** *	
Mi1.1	TTTATTCACTCATGACAAACTTTGATCTTGGATCTGGACTCTGGACTTACCTACCAGGGAG	984
Mi1.2	TTTATTCACTCATGACAAACTTTGATCTTGGCTCATGTTGGAACACTTACCCAGGGAG	984
Rpi-blb2	TTTATTCACTCATGACAAACTTTGATCTTGGCTCGGTGTTGAGCACTTACCCAGGGAG	1017
	***** *	
Mi1.1	GTATCAACTCTTGACGTGACTTTGGAAAGAGGAACCAAGGAATAAGAGGGTAATAACCAA	1044
Mi1.2	GTATCGACTCTTGACGTGACTTTGGAAAGAGAAATTAAAGGAATAAGAGGGTAATAACCAA	1044
Rpi-blb2	GTATCAACCTCTTGACCGGACTTTGGAAAGAGAAATTAAAGGATTAAAGAGGTACTGAGCAA	1077
	* *	
Mi1.1	ACAAATTGTGCAACCCCTAGACTTGTGGAAATTATTGAACCTCCTCAAGAAAGATCTCAA	1104
Mi1.2	ACAAATTGTGCAACCCCTAGACTTGTGGAAATTATTGAACCTCCTCAAGAAAGATCTCAA	1104
Rpi-blb2	ACAAATTGTGCAACCCCTAGTTCTGGAAAATTATTGAACCTCCTTAAGGAAGATCTCAA	1137
	***** *	
Mi1.1	CATGTTTATCTGAAAGGCCCTGGATTCACTCTCAATGTTGCTTCCCCTAGGAGTGTGGACCCA	1164
Mi1.2	CATGTTTATCTGAAAGGCCCAATTCACTCTCAATGTTGCTTCCCCTAGGAGTGTGGACCCA	1164

Rpi-blb2	CATGTTTATCTGAAAGTCCCCGATTCACTCATCTCAATATTGCTTCCCCATGAGTGATGGACCT	1197
Mi1.1	CTCTTCATGCATCTCACACTAACATACTTAAATGATTGATTCTAATGCTTATTCA	1224
Mi1.2	CTCTTCATGCATCTCACACTAACATGCACTTAATGATTGCTAGATTCTAATGCTTATTCA	1224
Rpi-blb2	CTCTTCATGCATCTGCCTACAGAGACACTTAGATGATTGCTGGATTCCAATGCTTATTCA	1257
	***** *	
Mi1.1	ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCTAAAGATCA	1284
Mi1.2	ATTTCCTTGTGATAAAGGAAGAAATCGAGTGGTGAAGTCAGAAACTGGAATTCTAAAGATCA	1284
Rpi-blb2	ATTGCTTTGATAAAGGAACAATGGCTGGTGAAGAAGACTTGAATCTAAAGATCT	1317
	***** *	
Mi1.1	TTCCTTGTGGATGGCTG-- AGCAAGGATTGTATAAAGATCTCTGGGCACGGTGTCTAGAT	1341
Mi1.2	TTCTTTGGGGATGGCTGCTGAGGATTGTGATAAAGATATCTGGGCACGGTGTCTAGAT	1344
Rpi-blb2	TTTTTGGCQAATATG -- AGCAAGGATTGTGATAAAGATCTCTGGGAACGGTGTCTAGAT	1374
	***** *	
Mi1.1	GTGGCTTATGAGGCAAAGATGTCATAGATTCAATTATTGTTGAGATAATGGTCTCTTA	1401
Mi1.2	GTGGCTTATGAGGCAAAGATGTCATAGATTCAATTATTGTTGAGATAATGGTCTCTTA	1404
Rpi-blb2	GTGGCATATGAGGCAAAGATGTCATAGATTCAATTATTGTTGAGATAATGGTCTCTTA	1434
	***** *	
Mi1.1	CATCTTATTCTCACTTCCCATACCATAAAGGAAGATCAAACCTTATCAAAGAAGAGATC	1461
Mi1.2	CATCTTATTCTCACTTCCCATACCATAAAGGAAGATCAAACCTTATCAAAGAAGAGATC	1464
Rpi-blb2	CATCTTATTCTCACTTCCCATACCATCAAAGGAAGATGATGCTTATCAAAGAAGGGTC	1494
	***** *	
Mi1.1	TCTGCTTTAGATGAGAACATCCCAAGGACAGAGGTCTAATCGTGTGAACCTCTCCCAAG	1521
Mi1.2	TCTGCTTTAGATGAGAACATCCCAAGGACAGAGGTCTAATCGTGTGAACCTCTCCCAAG	1524
Rpi-blb2	TCTGATTACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTGTGAACCTCTCCCAAG	1554

Mi1.1	AAACCAGTTGAGAGAAAGTCATTGACAACACTGATAAAAATTAACCTGTAGGTTTGAGGGAA	1581
Mi1.2	AAACCAGTTGAGAGAAAGTCATTGACAACACTGATAAAAATTAATTGTAGGTTTGAGGGAG	1584
Rpi-blb2	AAACCAGTTGAGAGCAAGTCATTGACAACACTGATAAAAATTAATTGTAGGTTTGAGGGAG	1614
	*****	*****
Mi1.1	ACAAAACTTGATACTTAGAAAGCTCACCCAGTGGATCGGCAGATCTAGATGTCAATTTCGATC	1641
Mi1.2	ACAAAACCTTGTATACTTAGAAAGCTCACCCAGTGGACCCGGAGATTAGATGTCAATTTCGATC	1644
Rpi-blb2	ACAAAACCTTGTATACTTAGAAAGCTCACCCAGTGGACCCGGAGATCTAGATGTCAATTTCGATC	1674
	*****	*****
Mi1.1	ACTGGTATGCCGGTTCAAGGTAAACACTACTTGGCATACAAAGTATAACATGATAAGTCA	1701
Mi1.2	ACCGGTATGCCGGTTCAAGGTAAACACTACTTGGCATACAAAGTATAACATGATAAGTCA	1704
Rpi-blb2	ATGGTATGCCGGTTCAAGGTAAACACTACTTGGCGTACACAAAGTATAACATGATAAAATCA	1734
	*****	*****
Mi1.1	GTTTCTAGCCGTTTCGACCTCGTGCATGGTCACGGTGCACGGCAAGGATGTGATGAGAAG	1761
Mi1.2	GTTCTAGACATTTGACCTCGTGCATGGTCACGGTGCATCAAGGATATGTGACGACAAG	1764
Rpi-blb2	GTTCCTAGCCATTCGACCTCGTGCATGGTCACGGTGCACGGTACACGAGAAG	1794
	*****	*****
Mi1.1	AAGTTGTGAAATACAATTTCAGTCAGTTAGTAGTCAGATTCAAATTGAGTGAAGAAT	1821
Mi1.2	AAGTTGTGAAATACAATTTCAGTCAGTTAGTAGGGCTCAGATTCAAATTGAGTGAAGAAT	1824
Rpi-blb2	AAGTTGTGAAATACAATTTCAGTCAGTTAGTAGGGCTCAGATTCAAATTGAGTGAAGAAT	1854
	*****	*****
Mi1.1	ATTGATGTTGCTGATAATTACGGAAACAAACTGTTGGAAAGAGGTTCTTATTGTCTTA	1881
Mi1.2	ATTGATGTTGCTGATAATTGGGGAAACAAACTGTTGGAAAGAGGTTCTTATTGTCTTA	1884
Rpi-blb2	ATTGATGTTGCTGATAAAACTACGGAAACAAATTGTGGAAAGAGGTTCTTATTGTCTTA	1914
	*****	*****

Mi1.1	GATGACCGTGTGGATACTACTACATGGGATGAGTTAACAAAGACCTTTCCCTGAATCTTAAG 1941
Mi1.2	GATGATGTGTGGATACTACTACATGGGATGAGTTGACAAGACCTTTCCCTGAAGCTTAAG 1944
Rpi-blb2	GATGACCGTGTGGATACTAATACATGGGATGAGCTAACAAAGACCTTTCCCTGAATGGTATG 1974

Mi1.1	AAAAGGAAGTAGGATTATTGACAACACTCGGGAAAAGGAAGTGGCTTGCATGGAAAGGCTG 2001
Mi1.2	AAAAGGAAGTAGGATTATTGACAACCTCGAGAAAAGGAAGTGGCTTGCATGGAAAGGCTG 2004
Rpi-blb2	AAAAGGAAGTAGAATTATTGACAACACTCGAGAAAAGGAAGTGGCTTGCATGGAAAGGCTC 2034

Mi1.1	AACACTGATCCTCTGACCTCGATTGCTAACGCCAGATGAAAGTTGGAACTATTAGAG 2061
Mi1.2	AACACTGATCCTCTGACCTCGATTGCTAACGCCAGATGAAAGTTGGAACTTTAGAT 2064
Rpi-blb2	TACACTGATCCTCTAACCTTCGATTGCTAACGATCAGAGAAAAGTTGGGAGTTATTAGAG 2094

Mi1.1	AAAAGGGCATTGGGAATGAGAGGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA 2121
Mi1.2	AAAAGGACATTGGTAATGAGAGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA 2124
Rpi-blb2	AAAAGGGCATTGGAAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGTAAAGAAATA 2154

Mi1.1	GCCGAAATTGTAAGGGCTTCCCTGGCTGATCTGATTGCTGGAGTCATTGCTGGG 2181
Mi1.2	GCCGAAATTGTAAGGGCTTCCCTGGCTGATCTGATTGCTGGAGTCATTGCTGGG 2184
Rpi-blb2	GCCGAAATTGTAAGGGCTTCCCTGGCTGATCTGATTGCTGGAGTCATTGCTGGG 2214

Mi1.1	AGGGAAAAGAAAAGGAGTGTGGCTTGAAGTCAAGTTGAGTTCTTTTATTTG 2241
Mi1.2	AGGGAAAAGAAAAGGAGTGTGGCTTGAAGTCAAGTTGAGTTCTTTTATTTG 2244
Rpi-blb2	AGGGAAAAGAAAAGGAGTGTGGCTTGAAGTGTAAATAATTGCAATTCTTTTATTTG 2274

Annotated Sheets Showing Changes

Mi1.1	AACAGTGAAGTGGAAAGTGTGAAAGTTATAGAATTAAAGTTATGACCATTACCATCAC	2301
Mi1.2	AACAGTGAAGTGGAAAGTGTGAAAGTTATAGAATTAAAGTTATGACCATTACCATCAC	2304
Rpi-blb2	AAGAATGAAGTGGAAAGTGTGAAAGTTATAGAATAAAAGTTATGACCACCTACCTGATCAC	2334
	***** * ***** *	
Mi1.1	CTCAAGCCATGCTTGCTGTATTGCAAGTTTCCGAAGGCACACTTCATTGACAATCTAT	2361
Mi1.2	CTCAAGCCATGCTTGCTTCACTTGGCAAGTTGGCCGAAGGCCACACTCCTTTGACAATCTAT	2364
Rpi-blb2	CTGAAGCCATGCTTGCTGTACTTTGCAAGTGTGCCGAAGGACTGGTAACGACAATCCAT	2394
	***** * ***** *	
Mi1.1	GAGTTGAATGTTTATTTCGGTGCTGAAGGGATTITGTGGAAAGACGGAGATGAACAGTATG	2421
Mi1.2	TTGTTTACTGTTATTGGGTGCTGAAGGATTGTGGAAAAGACGGAGATGAAGGGTATA	2424
Rpi-blb2	GAGTTGAACCTTATTGGGTTTGAAGGATTGTGGAAAAGACAGATATGAAGAGTCTG	2454
	***** *	
Mi1.1	GAAGAAGTGGTGAAGGATTATGGATGATTACAGTAGCTTGGTAATTGTGTTTC	2481
Mi1.2	GAAGAAGTGGTGAAGGATTATGGATGATTACAGTAGCTTGGTAATTGTGTTTC	2484
Rpi-blb2	GAGAAAGTGGTGAAAATTATTGGATGATTACAGTAGCTTGGTAATTGTGTTTC	2514
	***** *	
Mi1.1	AATGAGATAGGTTATGCACTGAATTTCAAATTCTGATCTTGTGCAATGACTTTGTGTTG	2541
Mi1.2	AATGAGATAGGTTATGCACTGAATTTCAAATTCTGATCTTGTGCAATGACTTTGTGTTG	2544
Rpi-blb2	AATGAGATAGGTTACCCCTACTTGCACACTCATGATCTTGTGCAATGACTTTGTGTTG	2574
	***** *	
Mi1.1	ATAAAAGCAAGAAAGGAAAATTGTGATCAGATAAGATCAAGTGCTCCATCAGATTG	2601
Mi1.2	ATAAAAGCAAGAAAGGAAAATTGTGATCAGATAAGATCAAGTGCTCCATCAGATTG	2604
Rpi-blb2	ATAAAAGCAAGAAAGGAAAAGTTGTGATCAGATAAGTTCAAGTGCTCCATCAGATTG	2634
	***** *	
Mi1.1	TTGCCTCGTCAAATTACCATGATTGATGAGGAGGAG--CACTTTGGCTTAATT	2658

Mi1.2	TGGCTCGTCAAATTACCATGATTATGAGGAGGAGCACTTGGCTTAATT	2664
Rpi-b1b2	TGCCACGTCAAATTAGCATGATTATGATGAGGCACTTGGCTTAATT	2694
	***** *	
Mi1.1	GTCATGTTCGATTCAAATAAGAAAGGCATTCTGGTAAACACCTTGGAGGATA	2718
Mi1.2	GTCATGTTCGATTCAAATAAGAAAGGCATTCTGGTAAACACCTTGGAGGATA	2724
Rpi-b1b2	GTCCTGTTGGTCAAATAAGAAAGGCATTCCGGTAAACACCTTGGAGGATA	2754
	*** ***	
Mi1.1	ATGGAGAACCGAGCTGGATGACAGTGTCTTGATGCATTCACCTAAGACA	2778
Mi1.2	ATGGAGAACCGAGCTGGATGACAGTGTCTTGATGCATTCACTTGAGGCTT	2784
Rpi-b1b2	AATGGAGATGAGCTGGACGACCATCTGGATACATTCATCTAAGACA	2814
	* *	
Mi1.1	CITAGAGTGTGGACCTGCATACGTCCTTATCATGGTGAAAGATTCTG	2838
Mi1.2	ATTAGAGTGTGGACCTGGAAACCCCTCTTAATCATGGTAATGGATTCT	2844
Rpi-b1b2	CTTAGAACCTTGACCTGGGAATCCTCTTATCATGGTTAAAGATTCTG	2874
	* *	
Mi1.1	ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACAAGT	2898
Mi1.2	ATATGCATGTTGAATCATTTGAGGTACTTAAGAACATTGGACACAAGT	2904
Rpi-b1b2	ATATGCATGTTGAATCATTTGAGGTACTTAAGCATTGGACAGAACAG	2934
	* *	
Mi1.1	TTGTCTTCTCAAACCTCTGGAAATCTAGAACGCCTGTTGCTACCAAC	2958
Mi1.2	TTCTCTTCTCAAACCTCTGGAAATCTAGAACGCTGTTGCTTAACAA	2964
Rpi-b1b2	TTGTCTTCTCAAACCTCTGGAAATCTAGAACGCTGTTGCTAACAA	2994
	* *	
Mi1.1	TTGGTACTATTACCGAGAATTGGATCTTGTAAAGTTGGCTCCGTTGGATGCT	3018
Mi1.2	TTGGTACTATTACCGAGAATTGGATCTTGTAAAGTTGGCTCCGTTGGGTGCT	3024

Rpi-blb2	TTGATACTATTACCGAGAATTGGGATCTTGTAAAGTTGCAAGTGTGTTACGGACTTGCT 3054
Mi1.1	TGTTCTTTGATATGGCATGAGATGAATTCATAATTGATAGCAGAGGACACAAGTTA 3078
Mi1.2	TGTTCTTTCTTGATATGGGATGGCAGATGAATTCATAATTGATAGCAAAGGACACAAGTTA 3084
Rpi-blb2	TGTTCTTTCTTGATATGGGATGGCAGATGAATTCATAACTGATAGCAGAGGACACAAGTTA 3114
	***** *
Mi1.1	GAGAACTTGAGAATATTAAACGGAACACTGTTGATTTCCATTTCGAAGATAACAAAGAATATT 3138
Mi1.2	GAGAACCTGAGAATATTAGGGGAACACTGTTGATTTCCATTTCGAAGATAACAAATGAAATATT 3144
Rpi-blb2	GAGAACCTTGCACAGCATTAGGGGAACCTGGCTTCCATTTCGAAGATAACAGAGGATATT 3174
	***** *
Mi1.1	TTCAAAAGGTTCCCAATCTTCAGTTGCTTCAATTGGAACCTCAAGGGAGTCATGGGATTAT 3198
Mi1.2	TTCAAAAGGTTCCCAATCTTCAGGTGCTTCAGTTGAACCTCAAGGGAGTCATGGGATTAT 3204
Rpi-blb2	TTCAAAAGGCTTCCCAATCTCAAGTGCCTTCATTCAAACTCAAGGGAGTCATGGGATTAT 3234
	***** *
Mi1.1	TCAACAGAGCAACATGGTTCTCGGAATTGGGATTTCCTAACTGAACTAGAAACACTCTCT 3258
Mi1.2	TCAACAGAGCAACATGGTTCCCGAAATTGGGATTGCCTAACTGAAACACTCTGT 3264
Rpi-blb2	TCAACAGAGCAATATTGGTTCCCGAAATTGGGATTCCATTAACTGAACTAGAAAACACTCACT 3294
	***** *
Mi1.1	GTAGGTTTAAAGTCAAACACAAACGATAGTGGGTCTCTGTAGCGACAAATGGGCCG 3318
Mi1.2	GTAGGTTTAAAGTCAAACACAAACCAACTGTGGGTCTCTGTGACAATGGGCCG 3324
Rpi-blb2	GTAGATTTGAAAGATCAACACAAATGACAGTGGGTCTCTGCAGCCATAAATGGCCA 3354
	***** *
Mi1.1	TGGGATTTCACCTCCCTCAAATTGAAATAACTGTGGTTGGTGAATTCCGCTGACA 3378
Mi1.2	TGGGATTTCACCTCCCTCAAATTGAAACTGTGGTTGTATGACTTTCCTCTGACA 3384
Rpi-blb2	TGGGATTTCACCTCCCTGAGTTGAAATTGCAATTGCTGACA 3414

Amendment dated October 24, 2007

Reply to Office Action of April 24, 2007

Annotated Sheets Showing Changes

Mi1.1	TCGATTCACTATAACAATAGCGAGACTGCCAACCTTGAAGAGTTGTCCTTATCAT	3438
Mi1.2	TCGATTCACTATAACAATAGCGAGACTGCCAACCTTGAAGAGTTGTCCTTATCAT	3444
Rpi-b1b2	TCGATTCACTATAACAATAGCGAGACTGCCAACCTTGAAGAGTTGTCCTTATCAT	3474
	***** * * * * *	*
Mi1.1	ACAATCATCCATGGAGAAGAATGGAAACATGGGGAGGAAGACACCTTGAAGAATCTCAA	3498
Mi1.2	ACAATCATCCAGGGAGAAGAATGGAAACATGGGGAGGAAGACACCTTGAAGAATCTCAA	3504
Rpi-b1b2	ACAATCATCCATGGGAAGAATGGAAACATGGAGAAGAACACCTTGAAGAATCTCAA	3534
	***** * * * * *	*
Mi1.1	TTTTGAACTTCAATCAAGTAGTATTCCAAGTGGGAGGGTTGGAGAGGAATCCTTCCCC	3558
Mi1.2	TTTTGAACTTGGCTTAAGTCACTGAACTTTCCAAGTGGGAGGTGGAGGAATCCTTCCCC	3564
Rpi-b1b2	TGTTGATGTTGAGTCAAAGTAGTCTTCCAAGTGGGAGGTGGAGGAATCTTTCCT	3594
	***** * * * * *	*
Mi1.1	AATCTTGAGAAATTAAACTGGGGATGTCATAAGCTAGAGGAGATTCCACCTAGTTT	3618
Mi1.2	AATCTTGAGAAATTAAACTGCAGGAATGTTGGTAAGCTGAGGAGATTCCACCTAGTTT	3624
Rpi-b1b2	ACGCTTGAGAAATTAGAAACTGTGGACTGTCTATAATCTGAGGAGATTCCGGTCTAGTTT	3654
	***** * * * * *	*
Mi1.1	GGAGATATTATTGAAATCTACAAATGTAAAGAGTCCTCAACTTGAAGATTCT	3678
Mi1.2	GGAGATATTATTGAAATTATCAAATGTAAAGAGTCCTCAACTTGAAGATTCT	3684
Rpi-b1b2	GGGGATATTATTCTTGAAAATTATCGAAACTGTAAAGGAGCCCTCAACTTGAAGATTCC	3714
	***** * * * * *	*
Mi1.1	GCTCTCAAAATTAGGAATACGCTGAAGATATGAGGGAGGGACGAGCTTCAGATCCTT	3738
Mi1.2	GCTCTCAAGATTAGAAATACGCTGAAGATATGAGGGAGGGAAACGATCTCAGATCCTT	3744
Rpi-b1b2	GCTCTCAAGATTAGGAATATGCTGAAGATATGAGGGAGGGACGAGCTTCAGATCCTT	3774
	***** * * * * *	*

Mi1.1	GGCCAAAAGAATAATCCCCTTATTAAAGTAG	3768
Mi1.2	GGCCAGAAGGAATAATCCCTTATTAAAGTAG	3774
Rpi-b1b2	GGCCAGAAGGATAATCCCGTTATTAAAGTAG	3804
***** * * * * *****		